

SEQUENCE LISTING

<110> Consejo Superior de Investigaciones Cientificas

<120> New Gene

<130> DGB/DE/PCT131

<140> PCT/GB99/03019

<141> 1999-09-10

<150> SE 9803069.5

<151> 1998-09-10

<150> US 60/100,873

<151> 1998-09-17

<160> 4

<170> PatentIn Ver. 2.1

<210> 1

<211> 2610

<212> DNA

<213> Homo sapiens

<220>

<223> This gene is referred to in the application as
Human Death Inducer Obliterator Gene 1. It has now
been named by the Human Gene Nomenclature
Committee as Death-Associated Transcription
Factor (DATF-1)

<400> 1

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<212> DNA

<213> Murine

<400> 2

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<212> PRT

<213> Homo sapiens

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Thr Ile Ala Lys Arg Glu Gly Ala Gly Asp Ala Glu Ala Asp Pro Leu
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Ser Thr Ala Val Lys Glu Arg Pro Ala Ser Ser Glu Lys Val Lys Gly
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Gly Asp Asp His Asp Asp Thr Ser Asp Ser Asp Ser Asp Gly Leu Thr

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Arg Glu Glu Gly Pro Ala Glu Thr Val Gly Ser Glu Ala Ser Asp Thr			
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Val Glu Gly Val Leu Pro Ser Lys Gln Glu Pro Glu Asn Asp Gln Gly			
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Cys Arg Gln Pro His Asn Asn Arg Phe Met Ile Cys Cys Asp Arg Cys			
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Cys Ile Leu Lys His Ala Ala Ala Thr Met Lys Phe Leu Ser Ser Gly			
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Lys Pro Ser Leu Pro Lys Cys Gly Ala Gln Ala Gly Ile Lys Ile Ser			

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 485 490 495
 Ala Cys Glu Ser Ser Thr Pro Ser Trp Ala Ser Asp His Asn Tyr Asn
 500 505 510
 Ala Val Lys Pro Glu Lys Thr Ala Ala Pro Ser Pro Ser Leu Leu Tyr
 515 520 525
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 Leu Cys

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 Arg Pro Leu Cys Lys Gln Glu Pro Glu Ala Ser Gln Gly Pro Val Ser
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 275 280 285
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 Glu Arg Asn Gly Glu Asp Tyr Ile Cys Pro Asn Cys Thr Ile Leu Gln
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 Cys Arg Ser Val Gly Ala Asp Gly Thr Asp Cys Thr Ser Ile Gly Thr
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 Val Glu Gln Lys Ser Gly Glu Asp Gln Gly Ile Lys Gly Arg Ile Glu
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 Val Val Glu Ala Pro Gly Ala Pro Lys Cys Ile Gly Pro Gly Cys Ser
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 Ser Val Ala Gln Pro Asp Ser Val Tyr Cys Ser Asn Asp Cys Ile Leu
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 Lys Thr Lys Pro Lys Glu Lys Val Lys Thr Lys Pro Glu Lys Phe Ser
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Leu Pro Lys Cys Ser Val Gln Val Gly Ile Lys Ile Ser Ser Val His
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Lys Arg Leu Ala Ser Glu Lys Arg Glu Asn Pro Val Lys Lys Val Met
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485 490 495

Ser Thr Pro Ser Trp Ala Ser Asp His Asn Tyr Asn Ala Val Lys Pro
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Glu Lys Pro Glu Lys Pro Thr Ala Leu Ser Pro Thr Leu Leu Ser Lys
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Cys Thr Tyr His Pro Lys Ala Gly Phe Pro Gly Pro Ser His His Leu
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Gly Gly Cys Leu Gly Leu Ser Arg Thr Arg Val Leu Gly Val Leu Val
545 550 555 560

Leu Ile Val Ala Ser Ser Ser Leu Pro Ala Arg Ser Arg Tyr Gln Asp
565 570 575

Ala Ser Gly Pro Gln Val Phe Leu Pro Ser Leu Trp Ser Leu Ser Gly
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Trp Phe Leu Lys Ser Cys Val Gly Leu Met Leu Glu Ala Ile Ser Tyr
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Phe Ser Phe Arg Pro Trp
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<223> Primer sequence

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26

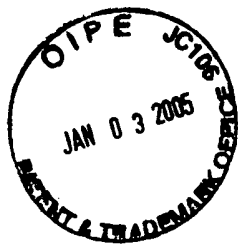
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<223> Additional N terminal cysteine for addition to a peptide
corresponding to amino acids 58-72 of murine DIO-1

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Consensus	
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Consensus	
	101	150
KIAA0333		
SEQ_ID_No3	SCPATDAETA SEGSVESASE TRSGPQSAST AVKERPASSE KVKGGDDHDD	
Consensus	
	151	200
KIAA0333		
SEQ_ID_No3	TSDSDSDGLT LKELQNLRR KREQEPTERP LKGIQSRLRK KRREEGPAET	
Consensus	
	201	250
KIAA0333		
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Consensus	ESKLEG KAAQDIKDEE
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KIAA0333		
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	401	450
KIAA0333		
SEQ_ID_No3	QVLEIAVSRS ISAFTHLHCI SCKVIEAPGA SKCIGPGCCH VAQPDSVYCS	
Consensus	-----	---VIEAPGA SKCIGPGCCH VAQPDSVYCS
	451	500
KIAA0333		
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Consensus	NDCILKHAAA TMKFLSSGKE QKPKPKEKMK MKPEKPSLPK CGAQAGIKIS	
	501	550
KIAA0333		
SEQ_ID_No3	SVHKRPAPPEK KETTVKKAVV VPARSEALGK EAACESSTPS WASDHNYNAV	
Consensus	SVHKRPAPPEK KETTVKKAVV VPARSEALGK EAACESSTPS WASDHNYNAV	
	551	600
KIAA0333		
SEQ_ID_No3	KPEKTAAPSP SLLYKSTKE- DRRSEEKAAA TAASKKTAPP GSTVGKQPAP	
Consensus	KPEKTAAPSP SLLYKCMYHL GVGLLDPSRS FWIAIPWACP GLGVAALC	KPEKTAAPSP SLLYKcmke. drrle#kaaa faaaiktAcP GlgVaaqc..

Alignment 1

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Consensus		
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Consensus		
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SEQ_ID_No3			
Consensus		
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SEQ_ID_No3			
Consensus		
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Alignment 1

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SEQ_ID_No3			
Consensus

Alignment 2

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SEQ_ID_No4 MDDKGHLSNE EAPKAIKPTS KEFRKTWGFR RTTIAKREGA GDTEADPSEQ
Consensus

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KIAA0333
SEQ_ID_No4 QPQQHNLSLR RSGRQPKRTE RVEEFLTTVR RRGKKNVPVS LEDSSEPTSS
Consensus

101 150
KIAA0333
SEQ_ID_No4 TVTDVETASE GSVESSEIR SGPVSDSLGK EHPASSEKAK GGEEEDTSD
Consensus

151 200
KIAA0333
SEQ_ID_No4 SDSA DGLTKE LQNRLRRKRE QEPVERSLRG SQNRLRKKRR EEDSAETGSV
Consensus

201 250
KIAA0333
SEQ_ID_No4 QIGSAEQDRP LCKQEPEASQ GPVSQSETDD IENQLEGKAT QGNTENPRE
Consensus EnqLEGKaa Qdnk#E#Pr#

251 300
KIAA0333
SEQ_ID_No4 LGRPKPECEG YDPNALYCIC RQPHNNRFMI CDRCEEFWFH GDCVGISEAR
Consensus aGrPKPECEg YDPNALYCIC RQPHNNRFMI CDRCEEFWFH GDCVGISEAR

301 350
KIAA0333
SEQ_ID_No4 GRLLERNGED YICPNCTILQ VQDETHSETA DQQA EAKWRPG DADGTDCTSI
Consensus GRLLERNGED YICPNCTILQ VQDETNGSAT NEQDSGCRSV GADGTDCTSI
GRLLERNGED YICPNCTILQ VQDETngeaa ##Q#agcRpg dADGTDCTSI

351 400
KIAA0333
SEQ_ID_No4 GTIEQKSSSED QGIKGRIEKA ANPSGKKKLK IFQPGPGPVP TQLPVLWQVL
Consensus GTVEQKSGED QGIKGRIEKA ANPSGKKKLK IFQP-----
GT!EQKSgED QGIKGRIEKA ANPSGKKKLK IFQP.....

401 450
KIAA0333
SEQ_ID_No4 EIAVRSRISA FTLLHCISCK VIEAPGASKC IGPGCCHVAQ PDSVYCSNDC
Consensus ----- VVEAPGAPKC IGPGCSSVAQ PDSVYCSNDC
..... V!EAPGApKC IGPGCchVAQ PDSVYCSNDC

451 500
KIAA0333
SEQ_ID_No4 ILKHAAATMK FLSSGKEQKP KPKEKMKMKP EKPSLPKCGA QAGIKISSVH
Consensus ILKHAAATMr FLSSGKEQKp KPKEKmkMkP EKfSLPKCga QaGIKISSVH

501 550
KIAA0333
SEQ_ID_No4 KRPAPEKKET TVKKAVVPA RSEALGKEAA CESSTPSWAS DHNYNAVKPE
Consensus KRLApEKrEn pVKK.Vmlaa RSEalGKEAA CESSTPSWAS DHNYNAVKPE

551 600
KIAA0333
SEQ_ID_No4 KTAAP---SP SLLYKSTKED RRSEKAAAT AASKKTAPPG STVGKQP--A
Consensus KPEKPTALSP TLLSKCTYHP KAGFPGPSHH LGGCLGLSRT RVLGVLVLIV
KpaaP...SP sLLsKcTked rageegaaah aagclgaprg rtlGkqp..a

Alignment 2

	601	650
KIAA0333	PRNLVPPKSS FANVAAATPA IKKPPSGFKG TIPKRPWLSA TPSSGASAAR	
SEQ_ID_No4	ASSSLPARSR YQDASGPQVF LPSLWSLSGW FLKSCVGLML EAIYSFSFRP	
Consensus	arnllParSr %a#aaaaqpa ikklpSgfgg fikkrpgLma eaiSgaSaar	
	651	700
KIAA0333	QAGPAPAAAT AASKKFPGSA ALVGAVRKPV VPSVPMASPA PGRLGAMSAA	
SEQ_ID_No4	W	
Consensus	q.....	
	701	750
KIAA0333	PSQPNSQIRQ NIRRLKEIL WKRVNDSDDL IMTENEVGKI ALHIEKEMFN	
SEQ_ID_No4		
Consensus	
	751	800
KIAA0333	LFQVTDNRYK SKYRSIMFNL KDPKNQGLFH RVLREEISLA KLVRLKPEEL	
SEQ_ID_No4		
Consensus	
	801	850
KIAA0333	VSKELSTWKE RPARSVMESR TKLHNESKKT APRQEAIPDL EDSPPVSDSE	
SEQ_ID_No4		
Consensus	
	851	900
KIAA0333	EQQESARAVP EKSTAPLLDV FSSMLKDTTS QHRAHLFDLN CKICTGQVPS	
SEQ_ID_No4		
Consensus	
	901	950
KIAA0333	AEDEPAPKKQ KLSASVKKED LSKKHDSSAP DPAPDSADDEV MPEAVPEVAS	
SEQ_ID_No4		
Consensus	
	951	1000
KIAA0333	EPGLESASHP NVDRTYFPGP PGDGHPEPSP LEDLSPCPAS CGSGVVTVT	
SEQ_ID_No4		
Consensus	
	1001	1050
KIAA0333	VSGRDPRTAP SSSCTAVASA ASRPDSTHMV EARQDVPKPV LTSVMVPKSI	
SEQ_ID_No4		
Consensus	
	1051	1100
KIAA0333	LAKPSSSPDP RYLSVPPSPN ISTSESRSPP EGDITLFLSR LSTIWKGFIN	
SEQ_ID_No4		
Consensus	
	1101	1150
KIAA0333	MQSVAKFVTK AYPVSGCFDY LSEDLPDTH IGGRIAPKTV WDYVGKLKSS	
SEQ_ID_No4		
Consensus	
	1151	1200
KIAA0333	VSKELCLIRF HPATEEEVA YISLYSYFSS RGRFGVVANN NRHVKDLYLI	
SEQ_ID_No4		
Consensus	

Alignment 2

	1201		1227
KIAA0333	PLSAQDPVPS	KLLPFEGPGK	RRLSGWR
SEQ_ID_No4			
Consensus